

1/6

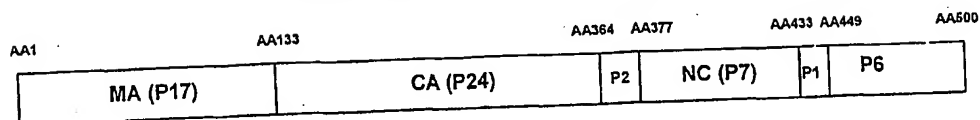
Gag (Pr55^{Gag}) polyprotein precursor

Figure 1

Matrix (MA) protein

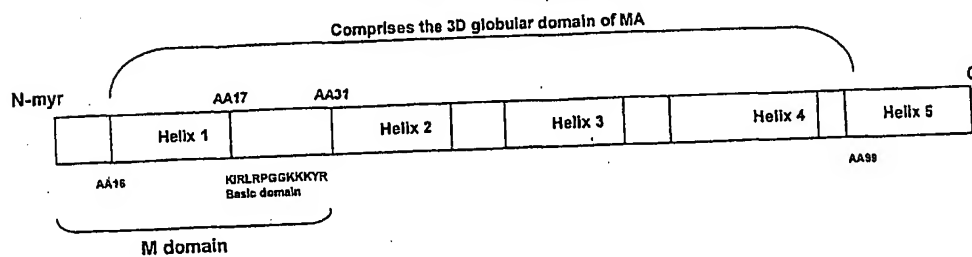


Figure 2

Nucleocapsid (NC) protein (p7)

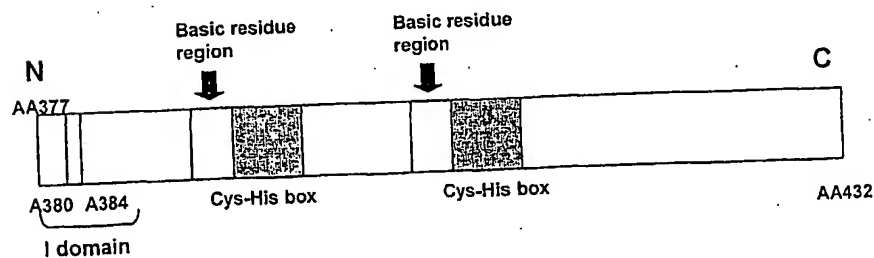


Figure 3

2/6

Capsid (CA) protein (p24)

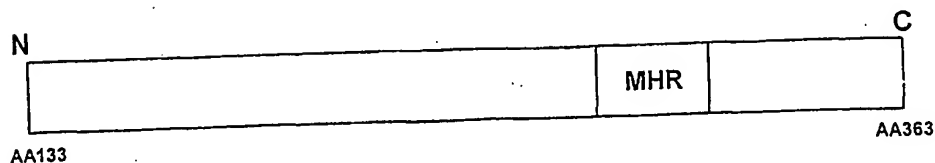
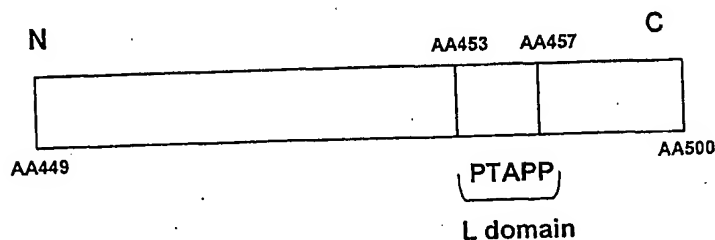


Figure 4

P6 protein



L domain

Figure 5

```

1  GAATTCATGG GTGCGAGAGC GTCAATATTA AGAGGGGAAA AATTAGATAA ATGGGAAAAG
61  ATTAGGTTAA GCCCAGGGGG AAAGAAACAT TATATGTTAA AACACATAGT ATGGGCGAGC
121  AGGGAGCTGG AAAGATTGCG ACTTAACCCCT GGCCCTTTAG AAACATCAGA AGGATGTAAA
181  CAAATAATGA AACAGCTACA ACCAGCTCTC CAGACAGGAA CAGAGGAAGT TAAATCATT
241  TACAACACAG TAGCAACTCT CTATTGTGTA CATGAAAAGA TAGAAGTACG AGACACCAAG
301  GAAGCCCTAG ATAAGATAGA GGAAGAACA AACAAATGTC AGCAAAAAAC GCAGCAGGCA
361  AAAGCGGCTG ACGGGAAAGT CAGTCAAAAT TATCCTATAG TCGAATCT CCAAGGGCAA
421  ATGGTACATC AAGCCATATC ACCTAGAACC TTGAATGCAT GGGTAAAGT AATAGAAGAA
481  AAGGCTTTTA GCCCAGAGGT AATACCCATG TTTACAGCAT TATCAGAAGG AGCCACCCCA
541  CAAGATTTAA ACACCATGTT AAATACAGTG GGGGACACC AAGCAGCCAT GCATATGTTA
601  AAAGATACTA TTAATGAAGA GGCTGCAGAA TGGGATAGAT TACATCCAGT CCATGCCGGG
661  CCTATTGCAC CAGGCCAGAT GAGAGAACA AGGGGAAGTG ACATAGCAGG AACTACTAGT
721  ACCCTTCAGG AACAAATAGC ATGGATGACA AGTAACCCAC CTATTCCAGT GGGAGACATC
781  TATAAAGAT GGATAATTCT GGGGTTAAAT AAAATAGTGA GAATGTATAG CCCGGTCAGC
841  ATTTTGGACA TAAGACAAGG GCCAAAGGAA CCCTTTCGAG ACTATCTAGA TCGGTTCTTT
901  AAAACTTTAA GAGCTGAACA AGCTACACAA GAAGTAAAAA ATTGGATGAC AGACACCTTG
961  TTAGTCCAAA ATGCGAACCC AGATTGTAAG ACCATTTTGA GAGCATTAGG ACCAGGGGCT
1021  ACATTAGAAG AAATGATGAC AGCATGTCAA GGGGTGGGAG GACCTGGCCA CAAAGCAAGA
1081  GTATTGGCTG AGGCAATGAG TCAACCAAAC AGTGGAAACA TAATGATGCA GAGAAGCAAT
1141  TTAAAGGCC CTAGAAGAA TGTAAATCT TTTAACTGTG GCAAGGAAGG GCACATAGCC
1201  AGAAATTGCA GAGCCCTAG GAAAGAAAGG TGTGGAAAT GTGGAAAAGA AGGACACCAA
1261  ATGAAAGACT GCACTGAGAG GCAGGCTAAT TTTTAGGGA AAATTTGGCC TTCCACCAAG
1321  GGGAGGCCAG GGAATTCCT TCAGACAGA CCAGAGCCAA CAGCCCCACC AGCAGAGAGC
1381  TTCAGGTPCG AAGAGCAAC CCCCCTCCG AAACAGGAGC CGATAGAAAG GGAACCCCTA
1441  ACTTCCCTCA AATCACTCTT TGGCAGCGAC CCCTGTCTC AATAAAAGTA GGGGGCCAGA
1501  CAAGGGAGGC TCTTTAGAC ACAGGAGCAG ATGATACAGT ATTGTGCAC

```

Figure 6

3/6

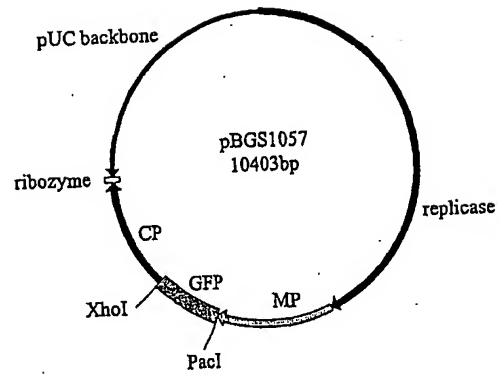


Figure 7

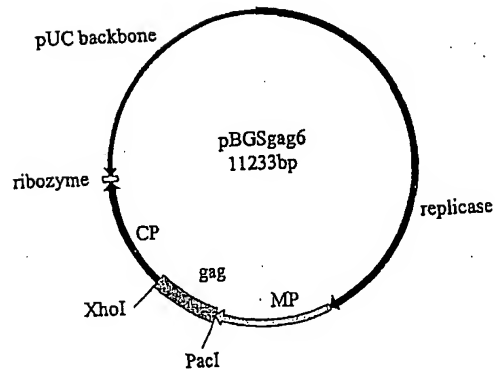


Figure 8

4/6

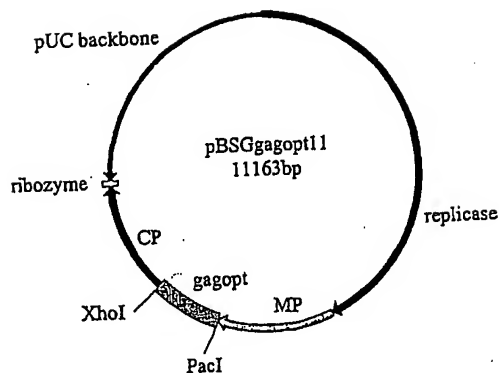


Figure 9

```

1      ATGGGTGCGA GAGCGTCAAT ATTAAGAGGG GAAAAATTAG ATAAATGGGA AAAGATTAGG
61     TTAAGGCCAG GGGGAAAGAA ACATTATATG TTAAACACA TAGTATGGGC GAGCAGGGAG
121    CTGGAAGAT  TTGCACTTAA CCCTGGCCTT TTAGAAACAT CAGAAGGATG TAAACAAATA
181    ATGAAACAGC TACAACCAGC TCTCCAGACA GGAACAGAGG AACTTAAATC ATTATACAAC
241    ACAGTAGCAA CTCTCTATTG TGTACATGAA AAGATAGAAG TACGAGACAC CAAGGAAGCC
301    TTAGATAAGA TAGAGGAAGA ACAAACAAA TGTCAGCAAA AAACGCAGCA GGCAAAAGCG
361    GCTGACGGGA AAGTCAGTCA AAATTATCCT ATAGTGCAGA ATCTCCAAGG GCAAATGGTA
421    CATCAAGCCA TATCACCTAG AACCTTGAAT GCATGGGTAA AAGTAATAGA AGAAAAGGCT
481    TTTAGCCCGAG AGTAATACC CATGTTTACA GCATTATCAG AAGGAGCCAC CCCACAAGAT
541    TTAAACACCA TGTTAAATAC AGTGGGGGGA CACCAAGCAG CCATGCAAAAT GTTAAAGAT
601    ACTATTAATG AAGAGGCTGC AGAATGGGAT AGATTACATC CAGTCCATGC GGGGCCTATT
661    GCACCAGGCC AGATGAGAGA ACCAAGGGGA AGTGACATAG CAGGAACTAC TAGTACCCTT
721    CAGGAACAAA TAGCATGGAT GACAAGTAAC CCACCTATTC CAGTGGGAGA CATCTATAAA
781    AGATGGATAA TTCTGGGGTT AAATAAAATA GTGAGAATGT ATAGCCCGGT CAGCATTTTG
841    GACATAAGAC AAGGGCCAAA GGAACCCTTT CGAGACTATG TAGATCGGTT CTTTAAACT
901    TTAAGAGCTG AACAAGCTAC ACAAGAAGTA AAAAATTGGA TGACAGACAC CTTGTTAGTC
961    CAAAATGCGA ACCCAGATTG TAAGACCATT TTGAGAGCAT TAGGACCAGG GGCTACATTA
1021   GAAGAAATGA TGACAGCATG TCAAGGGGTG GGAGGACCTG GCCACAAAGC AAGAGTATTG
1081   GCTGAGGCAA TGAGTCAAC AAACAGTGA AACATAATGA TGCAGAGAAG CAATTTTAAA
1141   GGCCCTAGAA GAATTGTTAA ATGTTTTAAC TGTGGCAAGG AAGGGCACAT AGCCAGAAAT
1201   TGCAGAGCCC CTAGGAAAAA AGGCTGTTGG AAATGTGGAA AAGAAGGACA CCAAATGAAA
1261   GACTGCACTG AGAGGCAGGC TAATTTTTTA GGGAAAATTT GGCCTTCCCA CAAGGGGAGG
1321   CCAGGGAATT TCCTTCAGAA CAGACCAGAG CCAACAGCCC CACCAGCAGA GAGCTTCAGG
1381   TTCGAAGAGA CAACCCCGC TCCGAAACAG GAGCCGATAG AAAGGGAACC CTTAACTTCC
1441   CTCAATCAC  TCTTTGGCAG CGACCCCTTG TCTCAATAA

```

Figure 10

5/6

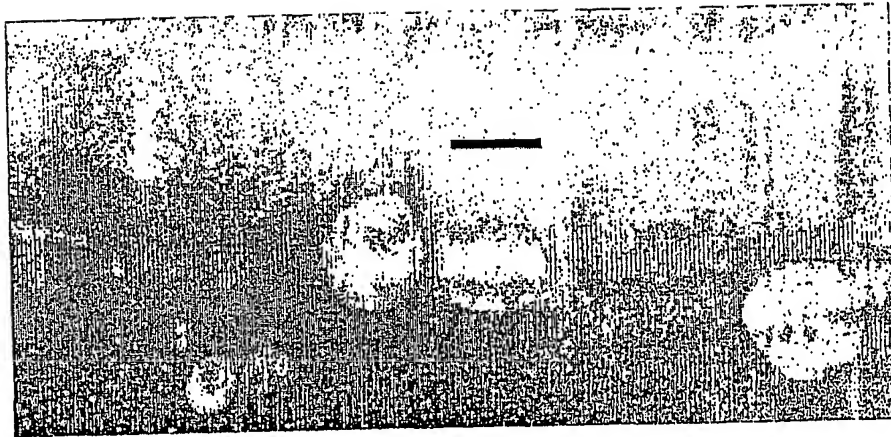


Figure 11

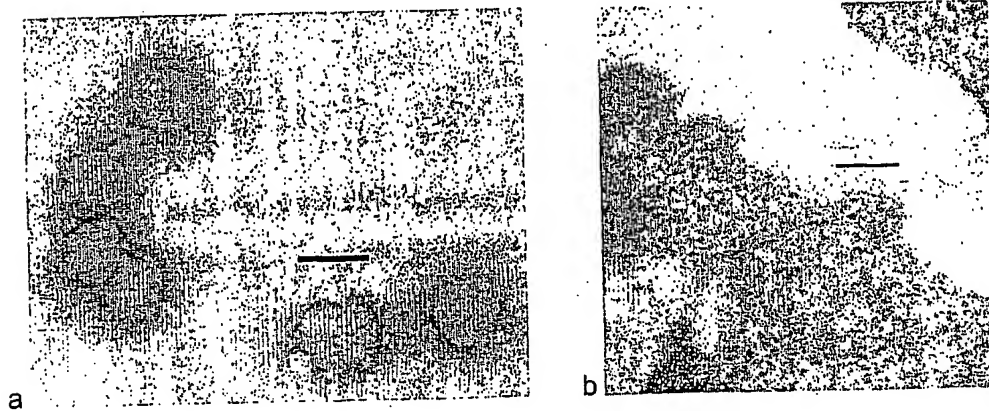


Figure 12

BEST AVAILABLE COPY

6/6

EFMGARASIL	RGEKLDKWEK	IRLRPGGKKH	YMLKHIVWAS	RELERFALNP	GLLETSEGCK	60
QIMKQLQPAL	QTGTEELKSL	YNTVATLYCV	HEKIEVRDTK	EALDKIEEEQ	NKCQKQTQQA	120
KAADGKVSQN	YPIVQNLOGQ	MVHQAI SPRT	LNAWVKVIEE	KAFSPEVIPM	FTALSEGATP	180
QDLNMTMLTV	GGHQAAMQML	KDTINEEAAE	WDRLHPVHAG	PIAPGQMREP	RGSDIAGTTS	240
TLQEQIAWMT	SNPPIPVGDI	YKRWIILGLN	KIVRMYSFVS	ILDIRQGPKE	PFRDYVDRFF	300
KTLRAEQATQ	EVKNWMTDTL	LVQANPDCK	TILRALGPGA	TLEEMMTACQ	GVGGPGHKAR	360
VLAEAMSQTN	SGNIMMQRSN	FKGFRRIVKC	FNCGKEGHIA	RNCRAPRKKG	CWKCGKEGHQ	420
MKDCTERQAN	FLGKIWP SHK	GRPGNFLQNR	PEPTAPPAES	FRFEETTPAP	KQEPIEREPL	480
TSLKSLFGSD	PLSQKGARQG	RLSTQEQMIQ	YCR			513

Figure 13

MGARASILRG	EKLDKWEKIR	LRPGGKKHYM	LKHIVWASRE	LERFALNPGL	LETSEGCKQI	60
MKQLQPALOT	GTEELKSLYN	TVATLYCVHE	KIEVRDTKEA	LDKIEEEQNK	CQKQTQAKA	120
ADGKVSQNY	IVQNLOGQMV	HQAISPRTL	AWVKVIEEKA	FSPEVIPMFT	ALSEGATPQD	180
LNTMLNTVGG	HQAAMQMLKD	TINEEAAEWD	RLHPVHAGPI	APGQMREPRG	SDIAGTTSTL	240
QEQIAWMTSN	PPIPVGDIYK	RWIILGLNKI	VRMYSFVSIL	DIRQGPKEPF	RDYVDRFFKT	300
LRAEQATQEV	KNWMTDTLLV	QANPDCKTI	LRLALGPGATL	EEMMTACQGV	GGPGHKARVL	360
AEAMSQTN SG	NIMMQRSNFK	GPERRIVKCFN	CGKEGHIARN	CRAPRKKGCW	KCGKEGHQMK	420
DCTERQANFL	GKIWP SHKGR	PGNFLQNRPE	PTAPPAESFR	FEETTPAPKQ	EPIEREPLTS	480
LKSLFGSDPL	SQ					

Figure 14